

Glu	Gln	Trp	Val 180	Asp	Tyr	Arg	Ala	Leu 185	Xaa	Gly	Asp	Pro	Ser 190	Asp	Asn
Leu	Pro	Gly 195	Val	Lys	Gly	Ile	Gly 200	Glu	Lys	Thr	Ala	Xaa 205	Lys	Leu	Leu
Xaa	Glu 210	Trp	Gly	Ser	Leu	Glu 215	Asn	Leu	Leu	Lys	Asn 220	Leu	Asp	Arg	Val
Lys 225	Pro	Xaa	Xaa	Arg	Glu 230	Lys	Ile	Xaa	Ala	His 235	Met	Glu	Asp	Leu	Xaa 240
Leu	Ser	Xaa	Xaa	Leu 245	Ser	Xaa	Val	Arg	Thr 250	Asp	Leu	Pro	Leu	Glu 255	Val
Asp	Phe	Ala	Xaa 260	Arg	Arg	Glu	Pro	Asp 265	Arg	Glu	Gly	Leu	Arg 270	Ala	Phe
Leu	Glu	Arg 275	Leu	Glu	Phe	Gly	Ser 280	Leu	Leu	His	Glu	Phe 285	Gly	Leu	Leu
Glu	Xaa 290	Pro	Lys	Ala	Leu	Glu 295	Glu	Ala	Pro	Trp	Pro 300	Pro	Pro	Glu	Gly
Ala 305	Phe	Val	Gly	Phe	Val 310	Leu	Ser	Arg	Pro	Glu 315	Pro	Met	Trp	Ala	Glu 320
Leu	Leu	Ala	Leu	Ala 325	Ala	Ala	Arg	Xaa	Gly 330	Arg	Val	His	Arg	Ala 335	Xaa
Asp	Pro	Leu	Xaa 340	Gly	Leu	Arg	Asp	Leu 345	Lys	Glu	Val	Arg	Gly 350	Leu	Leu
Ala	Lys	Asp 355	Leu	Ala	Val	Leu	Ala 360	Leu	Arg	Glu	Gly	Leu 365	Asp	Leu	Xaa
Pro	Gly 370	Asp	Asp	Pro	Met	Leu 375	Leu	Ala	Tyr	Leu	Leu 380	Asp	Pro	Ser	Asn
Thr 385	Thr	Pro	Glu	Gly	Val 390	Ala	Arg	Arg	Tyr	Gly 395	Gly	Glu	Trp	Thr	Glu 400
Asp	Ala	Gly	Glu	Arg 405	Ala	Leu	Leu	Ser	Glu 410	Arg	Leu	Phe	Xaa	Asn 415	Leu
Xaa	Xaa	Arg	Leu 420	Glu	Gly	Glu	Glu	Arg 425	Leu	Leu	Trp	Leu	Tyr 430	Xaa	Glu
Val	Glu	Lys 435	Pro	Leu	Ser	Arg	Val 440	Leu	Ala	His	Met	Glu 445	Ala	Thr	Gly
Val 450	Arg	Leu	Asp	Val	Ala	Tyr 455	Leu	Gln	Ala	Leu	Ser 460	Leu	Glu	Val	Ala
Glu 465	Glu	Ile	Arg	Arg	Leu 470	Glu	Glu	Glu	Val	Phe 475	Arg	Leu	Ala	Gly	His 480
Pro	Phe	Asn	Leu	Asn 485	Ser	Arg	Asp	Gln	Leu 490	Glu	Arg	Val	Leu	Phe 495	Asp
Glu	Leu	Gly	Leu 500	Pro	Ala	Ile	Gly	Lys 505	Thr	Glu	Lys	Thr	Gly 510	Lys	Arg

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240
GGGTACAAGG CGGGCCGGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC 300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC 360
GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG 480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG 540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC 600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG 660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG 720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGA CTTCGCC 780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC 840
AGCCTCCTCC ACGAGTTCGG CTTTCTGGAA AGCCCAAGG CCCTGGAGGA GGCCCCCTGG 900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC 960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT 1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG 1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC 1140
CTGGACCCTT CCAACACCAC CCCCAGAGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG 1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG 1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT 1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG 1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC 1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTTGA CGAGCTAGGG 1500